

SEQUENCE LISTING

<110> Japan Science and Technology Corporation

<120> A mast cell-specific adapter molecules and cDNAs thereof

<130> 00-F-047PCT/YS

<140> PCT/JP00/06351

<141> 2000-9-17

<150> JP11-263778

<151> 1999-09-17

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 1721

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (255) .. (1562)

<300>

<301> Goitsuka R., et al.

<302> A BASH/SLP-76-related adaptor protein MIST/Clink involved in IgE
receptor-mediated mast cell degranulation

<303> Int. Immunol.

<304> 12

<305> 4

<306> 573-580

<307> 2000

<308> GenBank/AB021220

<309> 2000-05-26

<400> 1

aagaggccaa actgccagg tctgtgctg cgtttctcg aaaacaaaa ctcaacaggc 60
acatacaagg cactctctgc tgaaggactc tctgagggg agagaacatg tcaactctat 120
cttacagagt gctccaggat gcgaccgtg accccctttc caggagctag ccgtctcaac 180
actgagccct tgactaaagg aagactgagc aggctgagtt gaagatccct ctcttttggc 240
aggtgccaaag gacc atg acc agc cag ggc aat aaa agg aca acg aaa gaa 290
Met Thr Ser Gln Gly Asn Lys Arg Thr Thr Lys Glu
1 5 10
gga ttc ggt gat ctg aga ttc cag aac gtc tct ctg ctg aaa aat agg 338
Gly Phe Gly Asp Leu Arg Phe Gln Asn Val Ser Leu Leu Lys Asn Arg
15 20 25
tca tgg cca agc ctc agc agt gcc aaa ggg cgg tgt cga gcg gtt ctg 386
Ser Trp Pro Ser Leu Ser Ser Ala Lys Gly Arg Cys Arg Ala Val Leu
30 35 40
gaa cca ctt ccg gat cac aga agg aac ttg gct ggg gtc cca ggt gga 434
Glu Pro Leu Pro Asp His Arg Arg Asn Leu Ala Gly Val Pro Gly Gly
45 50 55 60
gaa aaa tgc aac agt aac aac gac tac gaa gat cct gag ttc cag ctg 482
Glu Lys Cys Asn Ser Asn Asn Asp Tyr Glu Asp Pro Glu Phe Gln Leu
65 70 75
ctg aag gca tgg cca tca atg aaa att tta cca gcc aga cct atc cag 530

Leu	Lys	Ala	Trp	Pro	Ser	Met	Lys	Ile	Leu	Pro	Ala	Arg	Pro	Ile	Gln	
			80					85					90			
gaa	tcg	gaa	tac	gca	gat	aca	cgc	tat	ttc	cag	gat	atg	atg	gag	gct	578
Glu	Ser	Glu	Tyr	Ala	Asp	Thr	Arg	Tyr	Phe	Gln	Asp	Met	Met	Glu	Ala	
		95					100				105					
ccc	ctt	ctg	tta	cct	ccc	aag	gct	tct	gtc	tcc	act	gag	aga	caa	acc	626
Pro	Leu	Leu	Leu	Pro	Pro	Lys	Ala	Ser	Val	Ser	Thr	Glu	Arg	Gln	Thr	
	110					115					120					
agg	gat	gtg	agg	atg	aca	cag	ctg	gaa	gaa	gtg	gac	aag	cct	acc	ttc	674
Arg	Asp	Val	Arg	Met	Thr	Gln	Leu	Glu	Glu	Val	Asp	Lys	Pro	Thr	Phe	
125				130						135				140		
aag	gat	gtc	aga	agc	caa	cgc	ttt	aaa	gga	ttc	aaa	tac	aca	aaa	ata	722
Lys	Asp	Val	Arg	Ser	Gln	Arg	Phe	Lys	Gly	Phe	Lys	Tyr	Thr	Lys	Ile	
			145					150					155			
aac	aag	act	cct	ttg	cca	cct	cct	cgg	cct	gct	atc	act	ctc	ccc	aag	770
Asn	Lys	Thr	Pro	Leu	Pro	Pro	Pro	Arg	Pro	Ala	Ile	Thr	Leu	Pro	Lys	
		160						165					170			
aag	tac	caa	ccc	tta	ccc	cca	gca	cca	cca	gag	gag	agc	agt	gca	tac	818
Lys	Tyr	Gln	Pro	Leu	Pro	Pro	Ala	Pro	Pro	Glu	Glu	Ser	Ser	Ala	Tyr	
	175						180					185				
ttc	gct	cca	aag	ccc	acc	ttt	cca	gaa	gtc	cag	agg	ggg	ccc	agg	cag	866
Phe	Ala	Pro	Lys	Pro	Thr	Phe	Pro	Glu	Val	Gln	Arg	Gly	Pro	Arg	Gln	
	190					195					200					
agg	agt	gca	aaa	gac	ttc	agt	agg	gtc	ctt	gga	gca	gaa	gaa	gaa	tct	914
Arg	Ser	Ala	Lys	Asp	Phe	Ser	Arg	Val	Leu	Gly	Ala	Glu	Glu	Glu	Ser	
205				210						215				220		
cac	cac	cag	aca	aag	cca	gaa	tct	tct	tgc	cca	tca	tca	aac	caa	aac	962
His	His	Gln	Thr	Lys	Pro	Glu	Ser	Ser	Cys	Pro	Ser	Ser	Asn	Gln	Asn	

225 230 235
 ada cag aag agt cca cct gcc att gcc agc tct tcc tac atg cca gga 1010
 Thr Gln Lys Ser Pro Pro Ala Ile Ala Ser Ser Ser Tyr Met Pro Gly
 240 245 250
 aag cac agt ata caa gcc aga gac cat aca ggt agc atg cag cac tgt 1058
 Lys His Ser Ile Gln Ala Arg Asp His Thr Gly Ser Met Gln His Cys
 255 260 265
 cct gct cag aga tgc caa gct gca gcc agc cac agc cct cga atg ctg 1106
 Pro Ala Gln Arg Cys Gln Ala Ala Ala Ser His Ser Pro Arg Met Leu
 270 275 280
 ccc tat gaa aac aca aac tgc gag aaa cct gac ccc aca aag cct gat 1154
 Pro Tyr Glu Asn Thr Asn Ser Glu Lys Pro Asp Pro Thr Lys Pro Asp
 285 290 295 300
 gag aag gat gtc tgg cag aat gaa tgg tac att gga gaa tac agt cgc 1202
 Glu Lys Asp Val Trp Gln Asn Glu Trp Tyr Ile Gly Glu Tyr Ser Arg
 305 310 315
 cag gca gtg gaa gat gtg tta atg aaa gag aac aag gat ggt act ttt 1250
 Gln Ala Val Glu Asp Val Leu Met Lys Glu Asn Lys Asp Gly Thr Phe
 320 325 330
 ttg gtc cga gac tgc tct aca aaa tcc aag gca gaa cca tat gtt ttg 1298
 Leu Val Arg Asp Cys Ser Thr Lys Ser Lys Ala Glu Pro Tyr Val Leu
 335 340 345
 gtg gtg ttt tat ggg aac aag gtc tac aat gtg aaa atc cgt ttc ctc 1346
 Val Val Phe Tyr Gly Asn Lys Val Tyr Asn Val Lys Ile Arg Phe Leu
 350 355 360
 gag agc aat caa cag ttt gcc ctg ggc aca gga cta cga gga aat gag 1394
 Glu Ser Asn Gln Gln Phe Ala Leu Gly Thr Gly Leu Arg Gly Asn Glu
 365 370 375 380

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

5 / 13

```

atg ttt gat tct gtg gaa gac atc att gaa cac tac aca tat ttt ccc 1442
Met Phe Asp Ser Val Glu Asp Ile Ile Glu His Tyr Thr Tyr Phe Pro
      385                      390                      395
att ctg cta ata gat ggg aaa gac aag gct gca cgc agg aaa cag tgc 1490
Ile Leu Leu Ile Asp Gly Lys Asp Lys Ala Ala Arg Arg Lys Gln Cys
      400                      405                      410
tac ctc acc cag cca ctg cct ctc gcc agg ctc ctt ctc act cag tac 1538
Tyr Leu Thr Gln Pro Leu Pro Leu Ala Arg Leu Leu Leu Thr Gln Tyr
      415                      420                      425
tcc agc cag gca ctt cat gag taa gaagcccagc cagatatccc cgcattcagt 1592
Ser Ser Gln Ala Leu His Glu
      430                      435
gtctgggcct tgtctcattc ctggctcaat ggattcagtt cttcttccat ctgcatttat 1652
ctgcaaagta ttattttctg tgtcttcaag ggaatgatttt ttgactctgt aaaaaaaaaa 1712
aaaaaaaaaa 1721

```

<210> 2

<211> 435

<212> PRT

<213> Mus musculus

<400> 2

Met Thr Ser Gln Gly Asn Lys Arg Thr Thr Lys Glu Gly Phe Gly Asp
1 5 10 15
Leu Arg Phe Gln Asn Val Ser Leu Leu Lys Asn Arg Ser Trp Pro Ser
20 25 30
Leu Ser Ser Ala Lys Gly Arg Cys Arg Ala Val Leu Glu Pro Leu Pro
35 40 45

Gln Ala ~~Arg~~ Asp His Thr Gly Ser Met Gln His Cys Pro Ala Gln Arg

260

[illegible]

7/13

Cys Gln Ala Ala Ala Ser His Ser Pro Arg Met Leu Pro Tyr Glu Asn
275 280 285
Thr Asn Ser Glu Lys Pro Asp Pro Thr Lys Pro Asp Glu Lys Asp Val
290 295 300
Trp Gln Asn Glu Trp Tyr Ile Gly Glu Tyr Ser Arg Gln Ala Val Glu
305 310 315 320
Asp Val Leu Met Lys Glu Asn Lys Asp Gly Thr Phe Leu Val Arg Asp
325 330 335
Cys Ser Thr Lys Ser Lys Ala Glu Pro Tyr Val Leu Val Val Phe Tyr
340 345 350
Gly Asn Lys Val Tyr Asn Val Lys Ile Arg Phe Leu Glu Ser Asn Gln
355 360 365
Gln Phe Ala Leu Gly Thr Gly Leu Arg Gly Asn Glu Met Phe Asp Ser
370 375 380
Val Glu Asp Ile Ile Glu His Tyr Thr Tyr Phe Pro Ile Leu Leu Ile
385 390 395 400
Asp Gly Lys Asp Lys Ala Ala Arg Arg Lys Gln Cys Tyr Leu Thr Gln
405 410 415
Pro Leu Pro Leu Ala Arg Leu Leu Leu Thr Gln Tyr Ser Ser Gln Ala
420 425 430
Leu His Glu
435

<210> 3

<211> 1129

<212> DNA

<213> Homo sapiens

8/13

<220>

<221> CDS

<222> (1).. (1128)

<300>

<301> Goitsuka R., et al.

<302> A BASH/SLP-76-related adaptor protein MIST/Clink involved in IgE
receptor-mediated mast cell degranulation

<303> Int. Immunol.

<304> 12

<305> 4

<306> 573-580

<307> 2000

<308> GenBank/AB021220

<309> 2000-05-26

<400> 3

ttc cag aac ttc agt ctg cca aaa aac agg tca tgg cct cgc atc aat 48

Phe Gln Asn Phe Ser Leu Pro Lys Asn Arg Ser Trp Pro Arg Ile Asn

1 5 10 15

agt gcc aca ggc cag tac cag agg atg aac aag cct ctt cta gac tgg 96

Ser Ala Thr Gly Gln Tyr Gln Arg Met Asn Lys Pro Leu Leu Asp Trp

20 25 30

gaa aga aac ttt gct gca gtc ctg gat gga gca aaa ggc cac agt gat 144

Glu Arg Asn Phe Ala Ala Val Leu Asp Gly Ala Lys Gly His Ser Asp

35 40 45

gat gac tat gat gac cct gag ctt cgg atg gaa gag aca tgg cag tgg 192

Asp Asp Tyr Asp Asp Pro Glu Leu Arg Met Glu Glu Thr Trp Gln Ser

50 55 60

[illegible]

att aaa att tta cca gcc cgg cct ata aag gaa tct gaa tat gca gat	240
Ile Lys Ile Leu Pro Ala Arg Pro Ile Lys Glu Ser Glu Tyr Ala Asp	
65 70 75 80	
aca cac tat ttc aag gtt gca atg gac act ccc ctt ccg tta gac acc	288
Thr His Tyr Phe Lys Val Ala Met Asp Thr Pro Leu Pro Leu Asp Thr	
85 90 95	
agg acc tct atc tcc att gga cag ccg acc tgg aac aca cag acg agg	336
Arg Thr Ser Ile Ser Ile Gly Gln Pro Thr Trp Asn Thr Gln Thr Arg	
100 105 110	
ttg gaa aga gtg gac aaa ccc att tcc agg gac gtc aga agc caa aac	384
Leu Glu Arg Val Asp Lys Pro Ile Ser Arg Asp Val Arg Ser Gln Asn	
115 120 125	
att aaa gga gat gca tcc gta aga aag aac aag att cct tta cca cct	432
Ile Lys Gly Asp Ala Ser Val Arg Lys Asn Lys Ile Pro Leu Pro Pro	
130 135 140	
cct cgg cct ctc ata aca ctt ccg aag aag tac caa ccc ttg ccc cct	480
Pro Arg Pro Leu Ile Thr Leu Pro Lys Lys Tyr Gln Pro Leu Pro Pro	
145 150 155 160	
gag ccg gag agc agc agg cca cct tta tct cag aga cac acc ttt cca	528
Glu Pro Glu Ser Ser Arg Pro Pro Leu Ser Gln Arg His Thr Phe Pro	
165 170 175	
gaa gtc cag gga atg ccc agt cag ata agc tta agg gac tta agt gag	576
Glu Val Gln Gly Met Pro Ser Gln Ile Ser Leu Arg Asp Leu Ser Glu	
180 185 190	
gtc ctt gaa gca gaa aaa gtt cct cat aac cag agg aag cct gaa tca	624
Val Leu Glu Ala Glu Lys Val Pro His Asn Gln Arg Lys Pro Glu Ser	
195 200 205	
adt cat ctg tta gaa aac caa aat act caa gag att cca ctt gcc att	672

220

240

255

270

285

300

315

335

350

Ala Leu Gly Thr/Gly Leu Arg Gly Asp Glu Lys Phe Asp Ser Val Glu

11/13

355

360

365

gac atc atc gaa cac tac aag aat t

1129

Asp Ile Ile Glu His Tyr Lys Asn

370

375

<210> 4

<211> 376

<212> PRT

<213> Homo sapiens

<400> 4

Phe Gln Asn Phe Ser Leu Pro Lys Asn Arg Ser Trp Pro Arg Ile Asn

1

5

10

15

Ser Ala Thr Gly Gln Tyr Gln Arg Met Asn Lys Pro Leu Leu Asp Trp

20

25

30

Glu Arg Asn Phe Ala Ala Val Leu Asp Gly Ala Lys Gly His Ser Asp

35

40

45

Asp Asp Tyr Asp Asp Pro Glu Leu Arg Met Glu Glu Thr Trp Gln Ser

50

55

60

Ile Lys Ile Leu Pro Ala Arg Pro Ile Lys Glu Ser Glu Tyr Ala Asp

65

70

75

80

Thr His Tyr Phe Lys Val Ala Met Asp Thr Pro Leu Pro Leu Asp Thr

85

90

95

Arg Thr Ser Ile Ser Ile Gly Gln Pro Thr Trp Asn Thr Gln Thr Arg

100

105

110

Leu Glu Arg Val Asp Lys Pro Ile Ser Arg Asp Val Arg Ser Gln Asn

115

120

125

Ile Lys Gly Asp Ala Ser Val Arg Lys Asn Lys Ile Pro Leu Pro Pro

130 135 140
 Pro Arg Pro Leu Ile Thr Leu Pro Lys Lys Tyr Gln Pro Leu Pro Pro
 145 150 155 160
 Glu Pro Glu Ser Ser Arg Pro Pro Leu Ser Gln Arg His Thr Phe Pro
 165 170 175
 Glu Val Gln Gly Met Pro Ser Gln Ile Ser Leu Arg Asp Leu Ser Glu
 180 185 190
 Val Leu Glu Ala Glu Lys Val Pro His Asn Gln Arg Lys Pro Glu Ser
 195 200 205
 Thr His Leu Leu Glu Asn Gln Asn Thr Gln Glu Ile Pro Leu Ala Ile
 210 215 220
 Ser Ser Ser Ser Phe Thr Thr Ser Asn His Ser Val Gln Asn Arg Asp
 225 230 235 240
 His Arg Gly Gly Met Gln Pro Cys Ser Pro Gln Arg Cys Gln Pro Pro
 245 250 255
 Ala Ser Cys Ser Pro His Glu Asn Ile Leu Pro Tyr Lys Tyr Thr Ser
 260 265 270
 Trp Arg Pro Pro Phe Pro Lys Arg Ser Asp Arg Lys Asp Val Gln His
 275 280 285
 Asn Glu Trp Tyr Ile Gly Glu Tyr Ser Arg Gln Ala Val Glu Glu Ala
 290 295 300
 Phe Met Lys Glu Asn Lys Asp Gly Ser Phe Leu Val Arg Asp Cys Ser
 305 310 315 320
 Thr Lys Ser Lys Glu Glu Pro Tyr Val Leu Ala Val Phe Tyr Glu Asn
 325 330 335
 Lys Val Tyr Asn Val Lys Ile Arg Phe Leu Glu Arg Asn Gln Gln Phe
 340 345 350
 Ala Leu Gly Thr Gly Leu Arg Gly Asp Glu Lys Phe Asp Ser Val Glu

130 135 140
 145 150 155 160
 165 170 175
 180 185 190
 195 200 205
 210 215 220
 225 230 235 240
 245 250 255
 260 265 270
 275 280 285
 290 295 300
 305 310 315 320
 325 330 335
 340 345 350

375

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99																																																																																																																																																												
0	00000000	00000001	00000010	00000011	00000100	00000101	00000110	00000111	00001000	00001001	00001010	00001011	00001100	00001101	00001110	00001111	00010000	00010001	00010010	00010011	00010100	00010101	00010110	00010111	00011000	00011001	00011010	00011011	00011100	00011101	00011110	00011111	00100000	00100001	00100010	00100011	00100100	00100101	00100110	00100111	00101000	00101001	00101010	00101011	00101100	00101101	00101110	00101111	00110000	00110001	00110010	00110011	00110100	00110101	00110110	00110111	00111000	00111001	00111010	00111011	00111100	00111101	00111110	00111111	01000000	01000001	01000010	01000011	01000100	01000101	01000110	01000111	01001000	01001001	01001010	01001011	01001100	01001101	01001110	01001111	01010000	01010001	01010010	01010011	01010100	01010101	01010110	01010111	01011000	01011001	01011010	01011011	01011100	01011101	01011110	01011111	01100000	01100001	01100010	01100011	01100100	01100101	01100110	01100111	01101000	01101001	01101010	01101011	01101100	01101101	01101110	01101111	01110000	01110001	01110010	01110011	01110100	01110101	01110110	01110111	01111000	01111001	01111010	01111011	01111100	01111101	01111110	01111111	10000000	10000001	10000010	10000011	10000100	10000101	10000110	10000111	10001000	10001001	10001010	10001011	10001100	10001101	10001110	10001111	10010000	10010001	10010010	10010011	10010100	10010101	10010110	10010111	10011000	10011001	10011010	10011011	10011100	10011101	10011110	10011111	10100000	10100001	10100010	10100011	10100100	10100101	10100110	10100111	10101000	10101001	10101010	10101011	10101100	10101101	10101110	10101111	10110000	10110001	10110010	10110011	10110100	10110101	10110110	10110111	10111000	10111001	10111010	10111011	10111100	10111101	10111110	10111111	11000000	11000001	11000010	11000011	11000100	11000101	11000110	11000111	11001000	11001001	11001010	11001011	11001100	11001101	11001110	11001111	11010000	11010001	11010010	11010011	11010100	11010101	11010110	11010111	11011000	11011001	11011010	11011011	11011100	11011101	11011110	11011111	11100000	11100001	11100010	11100011	11100100	11100101	11100110	11100111	11101000	11101001	11101010	11101011	11101100	11101101	11101110	11101111	11110000	11110001	11110010	11110011	11110100	11110101	11110110	11110111	11111000	11111001	11111010	11111011	11111100	11111101	11111110	11111111